

## Exhibit A

BLAST 2 SEQUENCES alignment of SEQ ID NO: 3 with 12ge20305orf30, a hypothetical H. pylori ORF disclosed by Smith et al. in WO 96/40893.



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

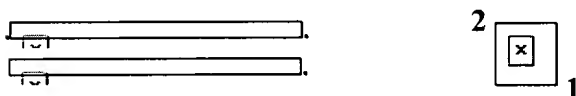
### BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match:  Mismatch:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  ☒ Filter

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Sequence 1 lcl|seq\_1 Length 759 (1 .. 759)

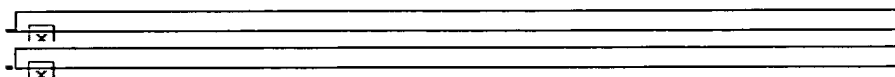
Sequence 2 lcl|seq\_2 Length 768 (1 .. 768)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1344 bits (699), Expect = 0.0  
Identities = 737/756 (97%)  
Strand = Plus / Plus



Query: 1 atggcatacaaatatgatagagacttgggaatttttaaagcaattggaatctagtgattta  
60  
Sbjct: 10 atggcatacaaatatgatagagacttgggaatttttaaagcaactggaatctagtgattta  
69

Query: 61 ttggatttggttgaggtgcttggttttggttaaagacggcgaaaaaagacacaatgaaaaa  
120  
Sbjct: 70 ttggatttggttcgaggtgcttggttttggttaaagacggcgaaaaaagacacaatgaaaaa  
129

Query: 121 ctgaccagctccatagaatacaaaaaggcatggcgatgattacgctaaatacgcagaaaaga  
180

Query: 181 atcgctgaagagttgcaatactatgggagcaatagttttgcgagtttcattaaaggcgaa  
240

Query: 241 ggagtcttatatacaaagagattttatgcgatgtgtgcgataaaattaaaggtcaattacaac  
300

Query: 301 aagaaaactgaaacgactttaattgaacaaaacatgcttttctaaaatcttagaaagaagt  
360

Query: 361 ttggaagaaatggatgatgaagaagtgaaagaaatgtgcgatgaattatccataaaaaaac  
420

Query: 421 acggacaattttaacagacaagccttaagcgcggcgactttaacgctgtttaaaatgggg  
480

Query: 481 ggtttttaaattcttatcaattagctgtcattgttgcaatgcggtcgcaaaaaccattcta  
540

Query: 541 gggcgtggtttatcgcttgcgggcaatcaggtgcttacaagaactctgagctttttaaca  
600

Query: 601 ggctcgtgttggtggatcattacaggcgtatggacagcgattgatattgcagggccggct  
660

|| ||||||||||||||||||||||||||||||||||||||||  
Sbjct: 610 ggccctgttggtggatcattacaggcgtatggacagcgattgatattgcagggccggct  
669

Query: 661 tatagggttaaccataccggcatgcattgtggttgccactttacgcctaaaaacacagcaa  
720

|||||||||||||||||||||||||||||||||||||| || |||  
Sbjct: 670 tatagggttaaccataccggcatgcattgtggtcgccactttacgcctaaaaacgcaacaa  
729

Query: 721 gccaatggagataagaagtcggttgcaaatagaatcc 756

|||||| ||||||||||||||||||||||||  
Sbjct: 730 gccaatgaagataagaagtcggttgcaaatagaatcc 765

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total  
secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Sequences: 1  
Number of Hits to DB: 166  
Number of extensions: 1  
Number of successful extensions: 1  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's gapped: 1  
Number of HSP's successfully gapped: 1  
Number of extra gapped extensions for HSPs above 10.0: 0  
Length of query: 759  
Length of database: 12,305,973,192  
Length adjustment: 26  
Effective length of query: 733  
Effective length of database: 12,305,973,166  
Effective search space: 9020278330678  
Effective search space used: 9020278330678  
Neighboring words threshold: 0  
Window for multiple hits: 0  
X1: 11 (21.1 bits)  
X2: 26 (50.0 bits)  
X3: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 21 (41.1 bits)

CODING SEQUENCE WITH HOMOLOGY TO SEQ ID NO: 3 DISCLOSED BY  
SMITH ET AL.

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 186778-60-9 REGISTRY  
CN DNA (Helicobacter pylori strain J99 open reading frame  
12ge20305orf30)  
(9CI) (CA INDEX NAME)  
FS NUCLEIC ACID SEQUENCE  
SQL 768  
NA 268 a 123 c 178 g 199 t  
NTE doublestranded

SEQ 1 aggaataata tggcatacaa atatgataga gacttgggaat ttttaaagca  
51 actggaatct agtgatztat tggatttggt cgagggtgctt gtttttggtta  
101 aagacggcga aaaaagacac aatgaaaaac tcacaagctc catagaatac  
151 aaaaggcatg gcgatgatta cgctaaatac gcagaaagaa tgcgtgaaga  
201 gttgcaatac tatgggagca atagttttgc gagtttcatt aaagggtgaag  
251 gagtcttata caaagagatt ttatgcatg tgtgcatgataa attaaagggtc  
301 aattacaaca agaaaactga aacgacttta attgaacaaa acatgctttc  
351 taaaatctta gaaagaagcc tagaagaaat ggatgatgaa gaagtgaag  
401 aaatgtgcga tgaattgtcc ataaaaaaca cggacaattt gaacagacaa  
451 gccttaagcg cggcgacttt aacgctgttt aaaatgggag gctttaaatc  
501 ttatcaatta gctgtcattg ttgcgaatgc gggttgcaaaa accattctag  
551 ggcgtgggtt atcgcttgcg ggcaatcaag tgcttacaag aactctgagc  
601 tttttaacag gccctgttgg ctggatcatt acaggcggtat ggacagcgat  
651 tgatattgca gggccggctt atagggtaac cataccggca tgcattgtgg  
701 tcgccacttt acgcctaaaa acgcaacaag ccaatgaaga taagaagtcg  
751 ttgcaaatag aatccggt

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological  
study);

PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

HP30 Coding Sequence, SEQ ID NO: 3

atggcatacaaatatgatagagacttggaatTTTTTaaagcaattggaatctagtgattta  
ttggatttggttgaggtgcttgTTTTTggtaaagacggcgaaaaaagacacaatgaaaaa  
ctgaccagctccatagaatacaaaaaggcatggcgatgattacgctaaatacgcagaaaga  
atcgctgaagagttgcaatactatgggagcaatagTTTTTgcgagtttcattaaaggcgaa  
ggagtcttatacaaaagagattttatgcgatgtgtgcgataaattaaagggtcaattacaac  
aagaaaactgaaacgactttaattgaacaaaacatgctttctaaaatcttagaaagaagt  
ttggaagaaatggatgatgaagaagtgaagaaatgtgcgatgaattatccataaaaaac  
acggacaatttaaacagacaagccttaagcgcggcgactttaacgctgtttaaagtggg  
ggTTTTTaaatcttatcaattagctgtcattgttgcaatgcggtcgcaaaaaccattcta  
gggcgtggtttatcgcttgcgggcaatcaggtgcttacaagaactctgagctTTTTTaa  
ggctcgttggtggatcattacaggcgtatggacagcgattgatattgcagggccggct  
tatagggttaaccataccggcatgcattgtggttgccactttacgcctaaaaacacagcaa  
gccaatggagataagaagtcggtgcaaatagaatccatt